

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/732,680A

DATE: 06/01/2001

TIME: 14:34:25

Input Set : A:\Mo6000- text.txt

Output Set: C:\CRF3\06012001\I732680A.raw

ENTERED

3 <110> APPLICANT: Bayer Aktiengesellschaft
5 <120> TITLE OF INVENTION: Nucleic acids coding for new acetylcholine receptor beta subunits of
6 insects
9 <130> FILE REFERENCE: Le A 34 147
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/732,680A
C--> 12 <141> CURRENT FILING DATE: 2001-05-10
14 <150> PRIOR APPLICATION NUMBER: DE 199 59 582.8
15 <151> PRIOR FILING DATE: 1999-12-10
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1539
23 <212> TYPE: DNA
24 <213> ORGANISM: Drosophila melanogaster
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (43)..(1365)
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31 attcggcacg aggggtacatc cgaaacaaag gcgcgctgaa ca atg acg acg act 54
32 Met Thr Thr Thr
33 1
35 ccc aag ata aag gca cca gtt tcc ggt cct gga ctg cca cta ctg ctg 102
36 Pro Lys Ile Lys Ala Pro Val Ser Gly Pro Gly Leu Pro Leu Leu Leu
37 5 10 15 20
39 caa atg cta atg ggg atg ctt ctt atg ggg ctg act tcc gtg cca ggc 150
40 Gln Met Leu Met Gly Met Leu Leu Met Gly Leu Thr Ser Val Pro Gly
41 25 30 35
43 gcc act gcc acc gcg gac ccc aag aac gcc aat gtc aag gcc ctg gat 198
44 Ala Thr Ala Thr Ala Asp Pro Lys Asn Ala Asn Val Lys Ala Leu Asp
45 40 45 50
47 cgc ctc cac gcc ggc ctg ttc acg aac tac gac agc gat gtg cag ccg 246
48 Arg Leu His Ala Gly Leu Phe Thr Asn Tyr Asp Ser Asp Val Gln Pro
49 55 60 65
51 gtg ttc caa gga acc ccc acg aac gtg tcc ctg gaa atg gtg gtc acc 294
52 Val Phe Gln Gly Thr Pro Thr Asn Val Ser Leu Glu Met Val Val Thr
53 70 75 80
55 tac ata gac atc gac gag ttg aac ggc aag ctg acc acc cac tgc tgg 342
56 Tyr Ile Asp Ile Asp Glu Leu Asn Gly Lys Leu Thr Thr His Cys Trp
57 85 90 95 100
59 ctg aat ctc cga tgg aga gac gag gag cgc gtg tgg caa ccg tca caa 390
60 Leu Asn Leu Arg Trp Arg Asp Glu Glu Arg Val Trp Gln Pro Ser Gln
61 105 110 115
63 tat gac aac atc acg cag atc act ttg aag tcc agc gag gtc tgg acc 438
64 Tyr Asp Asn Ile Thr Gln Ile Thr Leu Lys Ser Ser Glu Val Trp Thr
65 120 125 130
67 ccc caa atc aca ctc ttc aac ggc gac gaa ggt ggc ctg atg gcc gaa 486
68 Pro Gln Ile Thr Leu Phe Asn Gly Asp Glu Gly Gly Leu Met Ala Glu

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69	135	140	145	
71	acc cag gtg acc ctc agc cac gat ggc cac ttc cgg tgg atg cct cca	534		
72	Thr Gln Val Thr Leu Ser His Asp Gly His Phe Arg Trp Met Pro Pro			
73	150	155	160	
75	gcc gtg tac acg gcc tac tgc gaa ctc aac atg ctc aac tgg ccc cac	582		
76	Ala Val Tyr Thr Ala Tyr Cys Glu Leu Asn Met Leu Asn Trp Pro His			
77	165	170	175	180
79	gac aag cag agc tgc aag ttg aag atc ggc tcc tgg ggc ctg aag gtc	630		
80	Asp Lys Gln Ser Cys Lys Leu Lys Ile Gly Ser Trp Gly Leu Lys Val			
81	185	190	195	
83	gtc ctg ccg gag aac ggc acg gcg aga gga gag tcc ctt gac cac gac	678		
84	Val Leu Pro Glu Asn Gly Thr Ala Arg Gly Glu Ser Leu Asp His Asp			
85	200	205	210	
87	gac ctg gtt cag tca ccg gag tgg gaa atc gtg gac tcg cga gcc cac	726		
88	Asp Leu Val Gln Ser Pro Glu Trp Glu Ile Val Asp Ser Arg Ala His			
89	215	220	225	
91	ttt gtc agt cag gac tac tac ggc tac atg gag tac act ctg acg gct	774		
92	Phe Val Ser Gln Asp Tyr Tyr Gly Tyr Met Glu Tyr Thr Leu Thr Ala			
93	230	235	240	
95	cag cgg cgc tcc tcc atg tac acg gcc gtc atc tac aca ccc gcg tcc	822		
96	Gln Arg Arg Ser Ser Met Tyr Thr Ala Val Ile Tyr Thr Pro Ala Ser			
97	245	250	255	260
99	tgc atc gtc atc ctg gcc ctc tca gcc ttc tgg ctg cct ccc cac atg	870		
100	Cys Ile Val Ile Leu Ala Leu Ser Ala Phe Trp Leu Pro Pro His Met			
101	265	270	275	
103	ggc ggc gag aag atc atg atc aac ggc ctg ctc atc atc gtg atc gcc	918		
104	Gly Gly Glu Lys Ile Met Ile Asn Gly Leu Leu Ile Ile Val Ile Ala			
105	280	285	290	
107	gcc ttc ctc atg tac ttc gcc cag ctc ctg cca gtg ctg tcc aac aat	966		
108	Ala Phe Leu Met Tyr Phe Ala Gln Leu Leu Pro Val Leu Ser Asn Asn			
109	295	300	305	
111	act cca ctt gtg gta atc ttc tac agc acc agc ctg ctg tat ctg agc	1014		
112	Thr Pro Leu Val Val Ile Phe Tyr Ser Thr Ser Leu Leu Tyr Leu Ser			
113	310	315	320	
115	gtc tcc acc atc gtc gag gtt cta gtt ctg tac ctg gcc aca ggc aag	1062		
116	Val Ser Thr Ile Val Glu Val Leu Val Leu Tyr Leu Ala Thr Gly Lys			
117	325	330	335	340
119	cac aag agg cgc ctg ccg gag gcg ctg aga aag ctg ctg cac ggg cac	1110		
120	His Lys Arg Arg Leu Pro Glu Ala Leu Arg Lys Leu Leu His Gly His			
121	345	350	355	
123	ctg ggc acg tgg ctg ctg ctc tcg gtg ttc agc acc act ggc gag tcg	1158		
124	Leu Gly Thr Trp Leu Leu Leu Ser Val Phe Ser Thr Thr Gly Glu Ser			
125	360	365	370	
127	cag gcg gag aag acc aaa gag atg gac gag cac ccg tac gag gag gcg	1206		
128	Gln Ala Glu Lys Thr Lys Glu Met Asp Glu His Pro Tyr Glu Glu Ala			
129	375	380	385	
131	gac gag cag gag tcc agt ccg ctg ggc atc aac cac acc gag gtg ccg	1254		
132	Asp Glu Gln Glu Ser Ser Pro Leu Gly Ile Asn His Thr Glu Val Pro			
133	390	395	400	

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135 ggc gcc aag gcc aac cag ttc gac tgg gcg ctg ctg gcc acc gcc gtg 1302
136 Gly Ala Lys Ala Asn Gln Phe Asp Trp Ala Leu Leu Ala Thr Ala Val
137 405 410 415 420
139 gac cgc att tcc ttc gtt tcc ttc agc ctg gcc ttc ctc att ctg gcc 1350
140 Asp Arg Ile Ser Phe Val Ser Phe Ser Leu Ala Phe Leu Ile Leu Ala
141 425 430 435
143 atc agg tgc tcc gtg tagggatgct cgagactcaa ggccacatcc caagccagtg 1405
144 Ile Arg Cys Ser Val
145 440
147 cgcactctga actagtgtttg catttgcgat ttcattgtatt taatgtgtgt gcgaacttat 1465
149 aattattttaa tgatgagacc tcgatggaa taaaggacct ctgccgaatg tctgcttaca 1525
151 aaaaaaaaaa aaaa 1539
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 441
156 <212> TYPE: PRT
157 <213> ORGANISM: Drosophila melanogaster
159 <400> SEQUENCE: 2
160 Met Thr Thr Thr Pro Lys Ile Lys Ala Pro Val Ser Gly Pro Gly Leu
161 1 5 10 15
163 Pro Leu Leu Leu Gln Met Leu Met Gly Met Leu Leu Met Gly Leu Thr
164 20 25 30
166 Ser Val Pro Gly Ala Thr Ala Thr Ala Asp Pro Lys Asn Ala Asn Val
167 35 40 45
169 Lys Ala Leu Asp Arg Leu His Ala Gly Leu Phe Thr Asn Tyr Asp Ser
170 50 55 60
172 Asp Val Gln Pro Val Phe Gln Gly Thr Pro Thr Asn Val Ser Leu Glu
173 65 70 75 80
175 Met Val Val Thr Tyr Ile Asp Ile Asp Glu Leu Asn Gly Lys Leu Thr
176 85 90 95
178 Thr His Cys Trp Leu Asn Leu Arg Trp Arg Asp Glu Glu Arg Val Trp
179 100 105 110
181 Gln Pro Ser Gln Tyr Asp Asn Ile Thr Gln Ile Thr Leu Lys Ser Ser
182 115 120 125
184 Glu Val Trp Thr Pro Gln Ile Thr Leu Phe Asn Gly Asp Glu Gly Gly
185 130 135 140
187 Leu Met Ala Glu Thr Gln Val Thr Leu Ser His Asp Gly His Phe Arg
188 145 150 155 160
190 Trp Met Pro Pro Ala Val Tyr Thr Ala Tyr Cys Glu Leu Asn Met Leu
191 165 170 175
193 Asn Trp Pro His Asp Lys Gln Ser Cys Lys Leu Lys Ile Gly Ser Trp
194 180 185 190
196 Gly Leu Lys Val Val Leu Pro Glu Asn Gly Thr Ala Arg Gly Glu Ser
197 195 200 205
199 Leu Asp His Asp Asp Leu Val Gln Ser Pro Glu Trp Glu Ile Val Asp
200 210 215 220
202 Ser Arg Ala His Phe Val Ser Gln Asp Tyr Tyr Gly Tyr Met Glu Tyr
203 225 230 235 240
205 Thr Leu Thr Ala Gln Arg Arg Ser Ser Met Tyr Thr Ala Val Ile Tyr
206 245 250 255

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208 Thr Pro Ala Ser Cys Ile Val Ile Leu Ala Leu Ser Ala Phe Trp Leu
209                260                265                270
211 Pro Pro His Met Gly Gly Glu Lys Ile Met Ile Asn Gly Leu Leu Ile
212                275                280                285
214 Ile Val Ile Ala Ala Phe Leu Met Tyr Phe Ala Gln Leu Leu Pro Val
215                290                295                300
217 Leu Ser Asn Asn Thr Pro Leu Val Val Ile Phe Tyr Ser Thr Ser Leu
218 305                310                315                320
220 Leu Tyr Leu Ser Val Ser Thr Ile Val Glu Val Leu Val Leu Tyr Leu
221                325                330                335
223 Ala Thr Gly Lys His Lys Arg Arg Leu Pro Glu Ala Leu Arg Lys Leu
224                340                345                350
226 Leu His Gly His Leu Gly Thr Trp Leu Leu Leu Ser Val Phe Ser Thr
227                355                360                365
229 Thr Gly Glu Ser Gln Ala Glu Lys Thr Lys Glu Met Asp Glu His Pro
230                370                375                380
232 Tyr Glu Glu Ala Asp Glu Gln Glu Ser Ser Pro Leu Gly Ile Asn His
233 385                390                395                400
235 Thr Glu Val Pro Gly Ala Lys Ala Asn Gln Phe Asp Trp Ala Leu Leu
236                405                410                415
238 Ala Thr Ala Val Asp Arg Ile Ser Phe Val Ser Phe Ser Leu Ala Phe
239                420                425                430
241 Leu Ile Leu Ala Ile Arg Cys Ser Val
242                435                440

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246 <210> SEQ ID NO: 3

247 <211> LENGTH: 20

248 <212> TYPE: DNA

249 <213> ORGANISM: Artificial Sequence

251 <220> FEATURE:

252 <221> NAME/KEY: modified_base

253 <222> LOCATION: 9,12

254 <223> OTHER INFORMATION: Primer; n is i at positions 9 and 12

256 <400> SEQUENCE: 3

257 **tgccarccnt cncartayga**

20

260 <210> SEQ ID NO: 4

261 <211> LENGTH: 21

262 <212> TYPE: DNA

263 <213> ORGANISM: Artificial Sequence

265 <220> FEATURE:

266 <221> NAME/KEY: modified_base

267 <222> LOCATION: 13,16

268 <223> OTHER INFORMATION: Primer; n is i at positions 13 and 16

270 <400> SEQUENCE: 4

271 **catratytty tcncnccca t**

21

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4